

059.0
0814

CRF Errors Corrected by the STIC Systems Branch

OIRK

Serial Number:

09/915814

CRF Processing Date: 10/09/01
Edited by: MA
Verified by: (ST)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: **ENTERED**
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/9

OIPE

RAW SEQUENCE LISTING

DATE: 10/09/2001

PATENT APPLICATION: US/09/915,814

TIME: 10:40:24

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10092001\I915814.raw

3 <110> APPLICANT: Madeline M. Butler
 4 Andrew T. Watt
 5 Susan M. Freier
 6 Jacqueline Wyatt
 8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
 10 <130> FILE REFERENCE: ISPH-0587
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/915,814
 C--> 12 <141> CURRENT FILING DATE: 2001-07-26
 12 <160> NUMBER OF SEQ ID NOS: 230
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 20
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 20 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
 22 <400> SEQUENCE: 1
 23 tccgtcatcg ctctcaggg 20
 25 <210> SEQ ID NO: 2
 26 <211> LENGTH: 20
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
 33 <400> SEQUENCE: 2
 34 atgcattctg cccccaagga 20
 36 <210> SEQ ID NO: 3
 37 <211> LENGTH: 3804
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Homo sapiens
 41 <220> FEATURE:
 42 <221> NAME/KEY: CDS
 43 <222> LOCATION: (278)...(3508)
 45 <400> SEQUENCE: 3
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 47 aaagaggcac agaggttcatt acttagtggg ggccagctgt gatcggccaa ctgccagctg 120
 48 ccttaaaaag gaagaccagt gatgctagga tggagtgaag cccaagagga agtgccatca 180
 49 tgaggaatca atgagagatc tgtgaagaga gagggctggg tgggagccca gaaggataga 240
 50 acctggaaga tcaatatctc ccgtgagggg aataaca atg gag cca ggt tct aag 295
 51 Met Glu Pro Gly Ser Lys
 52 1 5
 54 tca gtg tct agg tca gac tgg caa cct gaa cca cac cag agg cct ata 343
 55 Ser Val Ser Arg Ser Asp Trp Gln Pro Glu Pro His Gln Arg Pro Ile
 56 10 15 20
 58 acc ccg cta gag cct ggg cca gaa aag aca ccc ata gcc cag cca gaa 391
 59 Thr Pro Leu Glu Pro Gly Pro Glu Lys Thr Pro Ile Ala Gln Pro Glu
 60 25 30 35
 62 tcg aag act ctg cag gga tcc aat acc caa cag aag cct gct tca aac 439

ENTERED

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63 Ser Lys Thr Leu Gln Gly Ser Asn Thr Gln Gln Lys Pro Ala Ser Asn
64      40                      45                      50
66 caa aga ccc ctc acc cag cag gag acc cct gca caa cat gat gct gaa 487
67 Gln Arg Pro Leu Thr Gln Gln Glu Thr Pro Ala Gln His Asp Ala Glu
68 55                      60                      65                      70
70 tcc cag aag gaa cct aga gcc caa caa aaa tct gct tca caa gag gaa 535
71 Ser Gln Lys Glu Pro Arg Ala Gln Gln Lys Ser Ala Ser Gln Glu Glu
72                      75                      80                      85
74 ttt ctt gcc cca cag aag ccc gca cca cag caa tca cct tac atc caa 583
75 Phe Leu Ala Pro Gln Lys Pro Ala Pro Gln Gln Ser Pro Tyr Ile Gln
76      90                      95                      100
78 agg gtg ctg ctc act caa cag gaa gct gcc tcc cag cag gga cct ggg 631
79 Arg Val Leu Leu Thr Gln Gln Glu Ala Ala Ser Gln Gln Gly Pro Gly
80      105                      110                      115
82 cta gga aaa gaa tct ata act caa cag gag cca gca ttg aga caa aga 679
83 Leu Gly Lys Glu Ser Ile Thr Gln Gln Glu Pro Ala Leu Arg Gln Arg
84      120                      125                      130
86 cat gta gcc cag cca ggg cct ggg cca gga gag cca cct cca gct caa 727
87 His Val Ala Gln Pro Gly Pro Gly Pro Gly Glu Pro Pro Pro Ala Gln
88 135                      140                      145                      150
90 caa gaa gct gaa tca aca cct gcg gcc cag gct aaa cct gga gcc aaa 775
91 Gln Glu Ala Glu Ser Thr Pro Ala Ala Gln Ala Lys Pro Gly Ala Lys
92      155                      160                      165
94 agg gag cca tct gcc ccg act gaa tct aca tcc caa gag aca cct gaa 823
95 Arg Glu Pro Ser Ala Pro Thr Glu Ser Thr Ser Gln Glu Thr Pro Glu
96      170                      175                      180
98 cag tca gac aag caa aca acg cca gtc cag gga gcc aaa tcc aag cag 871
99 Gln Ser Asp Lys Lys Gln Thr Thr Pro Val Gln Gly Ala Lys Ser Lys Gln
100      185                      190                      195
102 gga tct ttg aca gag ctg gga ttt cta aca aaa ctt cag gaa cta tcc 919
103 Gly Ser Leu Thr Glu Leu Gly Phe Leu Thr Lys Leu Gln Glu Leu Ser
104      200                      205                      210
106 ata cag cga tca gcc cta gag tgg aag gca ctt tct gag tgg gtc gca 967
107 Ile Gln Arg Ser Ala Leu Glu Trp Lys Ala Leu Ser Glu Trp Val Ala
108 215                      220                      225                      230
110 gat tct gag tca gaa tca gat gtg gga tca tct tca gac aca gat tct 1015
111 Asp Ser Glu Ser Glu Ser Asp Val Gly Ser Ser Ser Asp Thr Asp Ser
112      235                      240                      245
114 cca gcc acg atg ggt gga atg gtg gcc cag gga gtg aag cta ggc ttc 1063
115 Pro Ala Thr Met Gly Gly Met Val Ala Gln Gly Val Lys Leu Gly Phe
116      250                      255                      260
118 aaa gga aaa tct ggt tat aaa gtg atg tca gga tac agt ggg acg tcg 1111
119 Lys Gly Lys Ser Gly Tyr Lys Val Met Ser Gly Tyr Ser Gly Thr Ser
120      265                      270                      275
122 cca cat gag aaa acc agt gct cgg aat cac aga cac tac cag gat aca 1159
123 Pro His Glu Lys Thr Ser Ala Arg Asn His Arg His Tyr Gln Asp Thr
124      280                      285                      290
126 gcc tca agg ctc atc cac aac atg gac ctg cgc aca atg aca cag tcg 1207
127 Ala Ser Arg Leu Ile His Asn Met Asp Leu Arg Thr Met Thr Gln Ser

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132					315				320						325		
134	cct	ggg	gaa	acg	gcc	cag	cgg	ctg	tca	ggc	gtt	ttt	gcc	ggt	gta	cgg	1303
135	Pro	Gly	Glu	Thr	Ala	Gln	Arg	Leu	Ser	Gly	Val	Phe	Ala	Gly	Val	Arg	
136					330				335						340		
138	gag	cag	gcg	ctg	ggg	ctg	gag	ccg	gcc	ctg	ggc	cgc	ctg	ctg	ggt	gtg	1351
139	Glu	Gln	Ala	Leu	Gly	Leu	Glu	Pro	Ala	Leu	Gly	Arg	Leu	Leu	Gly	Val	
140					345				350						355		
142	gcg	cac	ctc	ttt	gac	ctg	gac	cca	gag	aca	ccg	gcc	aac	ggg	tac	cgc	1399
143	Ala	His	Leu	Phe	Asp	Leu	Asp	Pro	Glu	Thr	Pro	Ala	Asn	Gly	Tyr	Arg	
144		360						365					370				
146	agc	cta	gtg	cac	aca	gcc	cgc	tgc	tgc	ctg	gcg	cac	ctc	ctg	cac	aaa	1447
147	Ser	Leu	Val	His	Thr	Ala	Arg	Cys	Cys	Leu	Ala	His	Leu	Leu	His	Lys	
148	375					380					385					390	
150	tcc	cgc	tat	gtg	gcc	tcc	aac	cgc	cgc	agc	atc	ttc	ttc	cgc	acc	agc	1495
151	Ser	Arg	Tyr	Val	Ala	Ser	Asn	Arg	Arg	Ser	Ile	Phe	Phe	Arg	Thr	Ser	
152					395				400							405	
154	cac	aac	ctg	gcc	gag	ctg	gag	gcc	tac	ctg	gct	gcc	ctc	acc	cag	ctc	1543
155	His	Asn	Leu	Ala	Glu	Leu	Glu	Ala	Tyr	Leu	Ala	Ala	Leu	Thr	Gln	Leu	
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158	cgc	gct	ctg	gtc	tac	tac	gcc	cag	cgc	ctg	ctg	gtt	acc	aat	cgg	ccg	1591
159	Arg	Ala	Leu	Val	Tyr	Tyr	Ala	Gln	Arg	Leu	Leu	Val	Thr	Asn	Arg	Pro	
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163	Gly	Val	Leu	Phe	Phe	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Phe	Leu	
164		440					445						450				
166	cgg	gag	tat	gtc	acg	ctg	cat	aag	gga	tgc	ttc	tat	ggc	cgc	tgc	ctg	1687
167	Arg	Glu	Tyr	Val	Thr	Leu	His	Lys	Gly	Cys	Phe	Tyr	Gly	Arg	Cys	Leu	
168	455					460					465					470	
170	ggc	ttc	cag	ttc	acg	cct	gcc	atc	cgg	cca	ttc	ctg	cag	acc	atc	tcc	1735
171	Gly	Phe	Gln	Phe	Thr	Pro	Ala	Ile	Arg	Pro	Phe	Leu	Gln	Thr	Ile	Ser	
172				475					480						485		
174	att	ggg	ctg	gtg	tcc	ttc	ggg	gag	cac	tac	aaa	cgc	aac	gag	aca	ggc	1783
175	Ile	Gly	Leu	Val	Ser	Phe	Gly	Glu	His	Tyr	Lys	Arg	Asn	Glu	Thr	Gly	
176				490					495						500		
178	ctc	agt	gtg	gcc	gcc	agc	tct	ctc	ttc	acc	agc	ggc	cgc	ttt	gcc	atc	1831
179	Leu	Ser	Val	Ala	Ala	Ser	Ser	Leu	Phe	Thr	Ser	Gly	Arg	Phe	Ala	Ile	
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182	gac	ccc	gag	ctg	cgt	ggg	gct	gag	ttt	gag	cgg	atc	aca	cag	aac	ctg	1879
183	Asp	Pro	Glu	Leu	Arg	Gly	Ala	Glu	Phe	Glu	Arg	Ile	Thr	Gln	Asn	Leu	
184		520					525						530				
186	gac	gtg	cac	ttc	tgg	aaa	gcc	ttc	tgg	aac	atc	acc	gag	atg	gaa	gtg	1927
187	Asp	Val	His	Phe	Trp	Lys	Ala	Phe	Trp	Asn	Ile	Thr	Glu	Met	Glu	Val	
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191	Leu	Ser	Ser	Leu	Ala	Asn	Met	Ala	Ser	Ala	Thr	Val	Arg	Val	Ser	Arg	
192					555				560							565	

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198	ccc	acg	ctc	acg	gtc	acc	atc	tca	ccc	cca	ctg	gcc	cac	aca	ggc	cct	2071
199	Pro	Thr	Leu	Thr	Val	Thr	Ile	Ser	Pro	Pro	Leu	Ala	His	Thr	Gly	Pro	
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202	ggg	ccc	gtc	ctc	gtc	agg	ctc	atc	tcc	tat	gac	ctg	cgt	gaa	gga	cag	2119
203	Gly	Pro	Val	Leu	Val	Arg	Leu	Ile	Ser	Tyr	Asp	Leu	Arg	Glu	Gly	Gln	
204		600					605					610					
206	gac	agt	gag	gag	ctc	agc	agc	ctg	ata	aag	tcc	aac	ggc	caa	cgg	agc	2167
207	Asp	Ser	Glu	Glu	Leu	Ser	Ser	Leu	Ile	Lys	Ser	Asn	Gly	Gln	Arg	Ser	
208	615				620					625						630	
210	ctg	gag	ctg	tgg	cgg	cgc	ccc	cag	cag	gca	ccc	cgc	tgg	cgg	tcc	ctg	2215
211	Leu	Glu	Leu	Trp	Pro	Arg	Pro	Gln	Gln	Ala	Pro	Arg	Ser	Arg	Ser	Leu	
212				635						640				645			
214	ata	gtg	cac	ttc	cac	ggc	ggt	ggc	ttt	gtg	gcc	cag	acc	tcc	aga	tcc	2263
215	Ile	Val	His	Phe	His	Gly	Gly	Gly	Phe	Val	Ala	Gln	Thr	Ser	Arg	Ser	
216			650					655					660				
218	cac	gag	ccc	tac	ctc	aag	agc	tgg	gcc	cag	gag	ctg	ggc	gcc	ccc	atc	2311
219	His	Glu	Pro	Tyr	Leu	Lys	Ser	Trp	Ala	Gln	Glu	Leu	Gly	Ala	Pro	Ile	
220			665					670					675				
222	atc	tcc	atc	gac	tac	tcc	ctg	gcc	cct	gag	gcc	ccc	ttc	ccc	cgt	gcg	2359
223	Ile	Ser	Ile	Asp	Tyr	Ser	Leu	Ala	Pro	Glu	Ala	Pro	Phe	Pro	Arg	Ala	
224		680					685					690					
226	ctg	gag	gag	tgc	ttc	ttc	gcc	tac	tgc	tgg	gcc	atc	aag	cac	tgc	gcc	2407
227	Leu	Glu	Glu	Cys	Phe	Phe	Ala	Tyr	Cys	Trp	Ala	Ile	Lys	His	Cys	Ala	
228	695				700					705						710	
230	ctc	ctt	ggc	tca	aca	ggg	gaa	cga	atc	tgc	ctt	gcg	ggg	gac	agt	gca	2455
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232				715					720					725			
234	ggc	ggg	aac	ctc	tgc	ttc	acc	gtg	gct	ctt	cgg	gca	gca	gcc	tac	ggg	2503
235	Gly	Gly	Asn	Leu	Cys	Phe	Thr	Val	Ala	Leu	Arg	Ala	Ala	Ala	Tyr	Gly	
236			730						735					740			
238	gtg	cgg	gtg	cca	gat	ggc	atc	atg	gca	gcc	tac	ccg	gcc	aca	atg	ctg	2551
239	Val	Arg	Val	Pro	Asp	Gly	Ile	Met	Ala	Ala	Tyr	Pro	Ala	Thr	Met	Leu	
240			745					750						755			
242	cag	cct	gcc	gcc	tct	ccc	tcc	cgc	ctg	ctg	agc	ctc	atg	gac	ccc	ttg	2599
243	Gln	Pro	Ala	Ala	Ser	Pro	Ser	Arg	Leu	Leu	Ser	Leu	Met	Asp	Pro	Leu	
244		760					765						770				
246	ctg	ccc	ctc	agt	gtg	ctc	tcc	aag	tgt	gtc	agc	gcc	tat	gct	ggt	gca	2647
247	Leu	Pro	Leu	Ser	Val	Leu	Ser	Lys	Cys	Val	Ser	Ala	Tyr	Ala	Gly	Ala	
248	775				780					785						790	
250	aag	acg	gag	gac	cac	tcc	aac	tca	gac	cag	aaa	gcc	ctc	ggc	atg	atg	2695
251	Lys	Thr	Glu	Asp	His	Ser	Asn	Ser	Asp	Gln	Lys	Ala	Leu	Gly	Met	Met	
252				795						800					805		
254	ggg	ctg	gtg	cgg	cgg	gac	aca	gcc	ctg	ctc	ctc	cga	gac	ttc	cgc	ctg	2743
255	Gly	Leu	Val	Arg	Asp	Thr	Ala	Leu	Leu	Leu	Arg	Asp	Phe	Arg	Leu		
256			810						815					820			
258	ggt	gcc	tcc	tca	tgg	ctc	aac	tcc	ttc	ctg	gag	tta	agt	ggg	cgc	aag	2791

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259	Gly	Ala	Ser	Ser	Trp	Leu	Asn	Ser	Phe	Leu	Glu	Leu	Ser	Gly	Arg	Lys	
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263	Ser	Gln	Lys	Met	Ser	Glu	Pro	Ile	Ala	Glu	Pro	Met	Arg	Arg	Ser	Val	
264		840					845					850					
266	tct	gaa	gca	gca	ctg	gcc	cag	ccc	cag	ggc	cca	ctg	ggc	acg	gat	tcc	2887
267	Ser	Glu	Ala	Ala	Leu	Ala	Gln	Pro	Gln	Gly	Pro	Leu	Gly	Thr	Asp	Ser	
268	855					860				865						870	
270	ctc	aag	aac	ctg	acc	ctg	agg	gac	ttg	agc	ctg	agg	gga	aac	tcc	gag	2935
271	Leu	Lys	Asn	Leu	Thr	Leu	Arg	Asp	Leu	Ser	Leu	Arg	Gly	Asn	Ser	Glu	
272				875					880					885			
274	acg	tcg	tcg	gac	acc	ccc	gag	atg	tcg	ctg	tca	gct	gag	aca	ctt	agc	2983
275	Thr	Ser	Ser	Asp	Thr	Pro	Glu	Met	Ser	Leu	Ser	Ala	Glu	Thr	Leu	Ser	
276			890					895				900					
278	ccc	tcc	aca	ccc	tcc	gat	gtc	aac	ttc	tta	cca	cct	gag	gat	gca		3031
279	Pro	Ser	Thr	Pro	Ser	Asp	Val	Asn	Phe	Leu	Leu	Pro	Pro	Glu	Asp	Ala	
280		905					910					915					
282	ggg	gaa	gag	gct	gag	gcc	aaa	aat	gag	ctg	agc	ccc	atg	gac	aga	ggc	3079
283	Gly	Glu	Glu	Ala	Glu	Ala	Lys	Asn	Glu	Leu	Ser	Pro	Met	Asp	Arg	Gly	
284		920				925						930					
286	ctg	ggc	gtc	cgt	gcc	gcc	ttc	ccc	gag	ggt	ttc	cac	ccc	cga	cgc	tcc	3127
287	Leu	Gly	Val	Arg	Ala	Ala	Phe	Pro	Glu	Gly	Phe	His	Pro	Arg	Arg	Ser	
288	935			940				945				950					
290	agc	cag	ggt	gcc	aca	cag	atg	ccc	ctc	tac	tcc	tca	ccc	ata	gtc	aag	3175
291	Ser	Gln	Gly	Ala	Thr	Gln	Met	Pro	Leu	Tyr	Ser	Ser	Pro	Ile	Val	Lys	
292			955					960					965				
294	aac	ccc	ttc	atg	tcg	ccg	ctg	ctg	gca	ccc	gac	agc	atg	ctc	aag	agc	3223
295	Asn	Pro	Phe	Met	Ser	Pro	Leu	Leu	Ala	Pro	Asp	Ser	Met	Leu	Lys	Ser	
296		970					975					980					
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299	Leu	Pro	Pro	Val	His	Ile	Val	Ala	Cys	Ala	Leu	Asp	Pro	Met	Leu	Asp	
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303	Asp	Ser	Val	Met	Leu	Ala	Arg	Arg	Leu	Arg	Asn	Leu	Gly	Gln	Pro	Val	
304		1000				1005					1010						
306	acg	ctg	cgc	gtg	gtg	gag	gac	ctg	ccg	cac	ggc	ttc	ctg	acc	cta	gcg	3367
307	Thr	Leu	Arg	Val	Val	Glu	Asp	Leu	Pro	His	Gly	Phe	Leu	Thr	Leu	Ala	
308	1015			1020				1025				1030					
310	gcg	ctg	tgc	cgc	gag	acg	cgc	cag	gcc	gca	gag	ctg	tgc	gtg	gag	cgc	3415
311	Ala	Leu	Cys	Arg	Glu	Thr	Arg	Gln	Ala	Ala	Glu	Leu	Cys	Val	Glu	Arg	
312			1035					1040				1045					
314	atc	cgc	ctc	gtc	ctc	act	cct	ccc	gcc	gga	gcc	ggg	ccg	agc	ggg	gag	3463
315	Ile	Arg	Leu	Val	Leu	Thr	Pro	Pro	Ala	Gly	Ala	Gly	Pro	Ser	Gly	Glu	
316		1050					1055				1060						
318	acg	ggg	gct	gcg	ggg	gta	gac	ggg	ggc	tgc	ggg	ggg	cga	cac	taa		3508
319	Thr	Gly	Ala	Ala	Gly	Val	Asp	Gly	Gly	Cys	Gly	Gly	Arg	His			
320		1065				1070					1075						
322	aagcctgttg	ttcccatctg	cgccggcctc	cgctcatgaat	gccttccggg	ccgggcccga											3568
323	ggggacgcgg	gctgtgctta	cttaagtcgg	gggtggcaag	ggggcggggc	gggggcccga											3628

VERIFICATION SUMMARY

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DATE: 10/09/2001

TIME: 10:40:25

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10092001\I915814.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date